

**Amendments to the Specification:**

Please amend the paragraph at page page 7, beginning at line 1 to and including line 14 to read as follows:

--function are known in this art. Such variants are readily detected and predicted by algorithms used by those skilled in this art. For example, the well known BLAST algorithm (Altschul, S. F., *et al.* (1990) *J. Mol. Biol.* 215:403-410; ~~see also~~ <http://www.ncbi.nlm.nih.gov/BLAST/>) utilizes an amino acid substitution matrix to predict and evaluate tolerable amino acid substitution at residues of the query sequence. Accordingly, the skilled artisan appreciates the scope and meaning of the term "variant" when used to describe equivalent embodiments of a given polypeptide sequence. The term, "substitution mutant," as used herein, means a protein in which an amino acid residue is replaced with another amino acid residue. A human IL-18 "substitution mutant," as used herein, means a mutant that comprises from one to five amino acid substitutions in the sequence of SEQ ID NO:1, said substitutions being at an amino acid residue chosen from the group of: the cysteine at residue 38, the cysteine at residue 68, the cysteine at residue 76, the asparagine at residue 78, the glutamic acid at residue 121, the cysteine at residue 127, the leucine at residue 144, and the aspartic acid at residue 157.--